NCBI
Blast 2 Sequences results
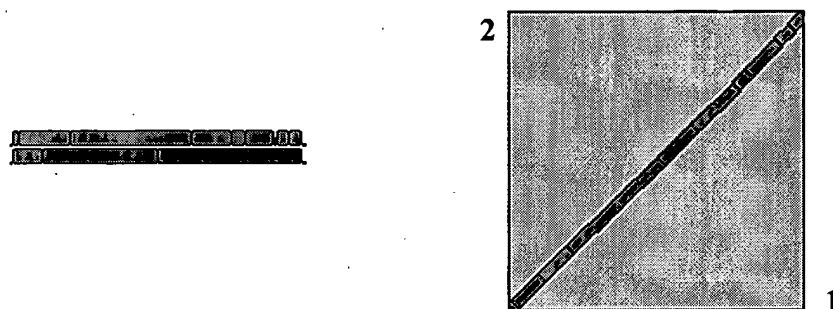
| PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure |

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix [BLOSUM62 ▼] gap open:[11] gap extension: [1]
x_dropoff: [50] expect:[10.0] wordsize: [3] Filter ☑ [Align]

Sequence 1 lcl|seq_1 **Length** 751 (1 .. 751)

Sequence 2 lcl|seq_2 **Length** 771 (1 .. 771)

Sema E
Sema D

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

```
Score =  708 bits (1827), Expect = 0.0
Identities = 339/757 (44%), Positives = 508/757 (66%), Gaps = 17/757 (2%)
```



```
Query: 4    RTICVLVGVFICSIC-VKGSSQPQARVYLTFDELRETKTSEYFSLSHHPLDYRILLMDED 62
            R +C+  GV + +      +      R+ L++ E+ E+      F+   +  Y   L+DE+
Sbjct: 6    RIVCLFWGVLLTARANYQNGKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEE 65

Query: 63   QDRIYVGSKDHILSLNINNISQEALSVFWPASTIKVEECKMAGKDPTHGCGNFVRVIQTF 122
            + R+YVG+KDHI S ++ NI ++   + WP S  +  +ECK AGKD    C NF++V++ +
Sbjct: 66   RSRLYVGAKDHIFSFDLVNI-KDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAY 124

Query: 123  NRTHLYVCGSGAFSPVCTYLNRGRRSEDQVFMID-SKCESGKGRCSFNPNVNTVSVMINE 181
            N+THLY CG+GAF P+CTY+   G    ED +F ++ S  E+G+G+  ++P + T S++I+
Sbjct: 125  NQTHLYACGTGAFHPICTYIEIGHHPEDNIFKLENSHFENGRGKSPYDPKLLTASLLIDG 184

Query: 182  ELFSGMYIDFMGTDAAIFRSLTKRNAVRTDQHNSKWLSEPMFVDAHVIPDGTDPNDAKVY 241
            EL+SG   DFMG D AIFR+L    + +RT+QH+S+WL++P F+ AH+I +   +P D KVY
Sbjct: 185  ELYSGTAADFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPKFISAHLISESDNPEDDKVY 244

Query: 242  FFFKEKLTDNNRSTKQIHSMIARICPNDTGGLRSLVNKWTTFLKARLVCSVTDEDGPETH 301
            FFF+E    D   S K  H+ I +IC ND GG RSLVNKWTTFLKARL+CSV   +G +TH
Sbjct: 245  FFFRENAIDGEHSGKATHARIGQICKNDFGGHRSLVNKWTTFLKARLICSVPGPNGIDTH 304

Query: 302  FDELEDVFLLETDNPRTTLVYGIFTTSSSVFKGSAVCVYHLSDIQTVFNGPFAHKEGPNH 361
            FDEL+DVFL+   +P+  +VYG+FTTSS++FKGSAVC+Y +SD++ VF GP+AH++GPN+
Sbjct: 305  FDELQDVFLMNFKDPKNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPNY 364

Query: 362  QLISYQGRIPYPRPGTCPGGAFTPNMRTTKEFPDDVVTFIRNHPLMYNSIYPIHKRPLIV 421
            Q + YQGR+PYPRPGTCP   F    +TK+ PDDV+TF R+HP MYN ++P++ RP+++
Sbjct: 365  QWVPYQGRVPYPRPGTCPSKTF-GGFDSTKDLPDDVITFARSHPAMYNPVFPMNNRPIVI 423
```

```
Query:  422 RIGTDYKYTKIAVDRVNAADGRYHVLFLGTDRGTVQKVVVLPTNNSVS-GELILEELEVF 480
                +   +Y++T+I VDRV+A DG+Y V+F+GTD GTV KVV +P        E++LEE+ VF
Sbjct:  424 KTDVNYQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSIPKETWYDLEEVLLEEMTVF 483


Query:  481 KNHAPITTMKISSKKQQLYVSSNEGVSQVSLHRCHIYGTACADCCLARDPYCAWDGHSCS 540
                +   I+ M++S+K+QQLY+ S  GV+Q+ LHRC IYG ACA+CCLARDPYCAWDG +CS
Sbjct:  484 REPTAISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAWDGSACS 543


Query:  541 RFYPTGKRRSRRQDVRHGNPLTQCRGFNLKAY--RNAAEIVQYGVKNNTTFLECAPKSPQ 598
             R++PT KRR+RRQD+R+G+PLT C    +   +   E + YGV+N++TFLEC+PKS +
Sbjct:  544 RYFPTAKRRTRRQDIRNGDPLTHCSDLHHDNHHGHSPEERIIYGVENSSTFLECSPKSQR 603


Query:  599 ASIKWLLQ-KDKDRRKEVKLNERIIATSQGLLIRSVQGSDQGLYHCIATENSFKQTIAKI 657
             A + W  Q ++++R++E+++++ II T QGLL+RS+Q  D G Y C A E+ F QT+ K+
Sbjct:  604 ALVYWQFQRRNEERKEEIRVDDHIIRTDQGLLLRSLQQKDSGNYLCHAVEHGFIQTLLKV 663


Query:  658 NFKVLDSEMVAVVTDKWSPWTWA-------SSVRALPFHPKDIMGAFSHSEMQMINQYCK 710
              +V+D+E + + K       +    S + +D M +H + ++++C+
Sbjct:  664 TLEVIDTEHLEELLHKDDDGDGSKTKEMSNSMTPSQKVWYRDFMQLINHPNLNTMDEFCE 723


Query:  711 DT--RQQHQQGDESQKMRGDYGKLKALINSRKSRNRR 745
                R + Q+      G+  K K L ++K RNRR
Sbjct:  724 QVWKRDRKQRRQRPGHTPGNSNKWKHLQENKKGRNRR 760


CPU time:     0.04 user secs.        0.01 sys. secs        0.05 total secs.

Lambda      K        H
   0.321    0.135    0.413

Gapped
Lambda      K        H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 4866
Number of Sequences: 0
Number of extensions: 399
Number of successful extensions: 8
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 751
length of database: 479,146,392
effective HSP length: 135
effective length of query: 616
effective length of database: 479,146,257
effective search space: 295154094312
effective search space used: 295154094312
T: 9
A: 40
X1: 16 ( 7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 79 (35.0 bits)
```